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Page 1 of 7

1696



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/875,221B

DATE: 11/13/2002

TIME: 15:45:04

#16

Input Set : A:\Carp0089.ST25.txt

Output Set: N:\CRF4\11132002\I875221B.raw

3 <110> APPLICANT: Athwal, Diljeet Singh  
4 Brown, Derek Thomas  
5 Weir, Andrew Neil Charles  
6 Popplewell, Andrew George  
7 Chapman, Andrew Paul  
8 King, David John  
10 <120> TITLE OF INVENTION: Biological Products  
12 <130> FILE REFERENCE: Carp-0089  
14 <140> CURRENT APPLICATION NUMBER: 09/875,221B  
15 <141> CURRENT FILING DATE: 2001-06-06  
17 <150> PRIOR APPLICATION NUMBER: GB0013810.7  
18 <151> PRIOR FILING DATE: 2000-06-06  
20 <160> NUMBER OF SEQ ID NOS: 130  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 5  
26 <212> TYPE: PRT  
27 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: hTNF40 CDRH1  
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35 1 5  
38 <210> SEQ ID NO: 2  
39 <211> LENGTH: 17  
40 <212> TYPE: PRT  
41 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: hTNF40/human hybrid CDRH2  
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49 1 5 10 15  
52 Gly  
56 <210> SEQ ID NO: 3  
57 <211> LENGTH: 9  
58 <212> TYPE: PRT  
59 <213> ORGANISM: Artificial Sequence  
61 <220> FEATURE:  
62 <223> OTHER INFORMATION: hTNF40 CDRH3  
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66 Gly Tyr Arg Ser Tyr Ala Met Asp Tyr  
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## RAW SEQUENCE LISTING

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Input Set : A:\Carp0089.ST25.txt

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95 1          5
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101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
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108 Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
109 1          5
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114 <212> TYPE: PRT
115 <213> ORGANISM: Artificial Sequence
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123 1          5          10          15
126 Gly
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131 <211> LENGTH: 321
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
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138 <220> FEATURE:
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141 <223> OTHER INFORMATION:
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146 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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48

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149 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac      96
150 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
151          20          25          30
153 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc      144
154 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
155          35          40          45
157 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga      192
158 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
159          50          55          60
161 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca      240
162 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
163 65          70          75          80
165 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc      288
166 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
167          85          90          95
169 aca ttc ggt cag ggt act aaa gta gaa atc aaa      321
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176 <212> TYPE: PRT
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179 <220> FEATURE:
180 <223> OTHER INFORMATION: hTF40-gL1
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189          20          25          30
192 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
193          35          40          45
196 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
197          50          55          60
200 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
201 65          70          75          80
204 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
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209          100          105
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220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (1)..(321)

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Input Set : A:\Carp0089.ST25.txt

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229 1 5 10 15

231 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96

232 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn

233 20 25 30

235 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc 144

236 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

237 35 40 45

239 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192

240 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly

241 50 55 60

243 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240

244 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

245 65 70 75 80

247 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288

248 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu

249 85 90 95

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253 100 105

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259 <213> ORGANISM: Artificial Sequence

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264 <400> SEQUENCE: 11

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267 1 5 10 15

270 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn

271 20 25 30

274 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

275 35 40 45

278 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly

279 50 55 60

282 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

283 65 70 75 80

286 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu

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290 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

291 100 105

294 <210> SEQ ID NO: 12

295 <211> LENGTH: 354

296 <212> TYPE: DNA

297 <213> ORGANISM: Artificial Sequence

299 <220> FEATURE:

## RAW SEQUENCE LISTING

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Input Set : A:\Carp0089.ST25.txt

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300 <223> OTHER INFORMATION: ghlhTNF40.4 (Figure 10)
302 <220> FEATURE:
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304 <222> LOCATION: (1)..(354)
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311 1          5          10          15
313 tcc gtc aaa gtt tgc tgt aag gcc tca ggc tac gtg ttc aca gac tat      96
314 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
315          20          25          30
317 ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg      144
318 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
319          35          40          45
321 ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc      192
322 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
323          50          55          60
325 cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac      240
326 Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
327 65          70          75          80
329 atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt      288
330 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
331          85          90          95
333 gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc      336
334 Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
335          100          105          110
337 cta gtc aca gtc tcc tca      354
338 Leu Val Thr Val Ser Ser
339          115
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344 <212> TYPE: PRT
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347 <220> FEATURE:
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350 <400> SEQUENCE: 13
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357          20          25          30
360 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
361          35          40          45
364 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
365          50          55          60
368 Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
369 65          70          75          80
372 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
373          85          90          95

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